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RAW SEQUENCE LISTING

DATE: 03/11/2002 \

PATENT APPLICATION: US/09/559,021A

TIME: 09:51:12

Input Set : A:\Mirus.014.02.ST25.txt

Output Set: N:\CRF3\03112002\I559021A.raw

#15

3 <110> APPLICANT: WOLFF, JON
 4 SOKOLOFF, ALEXANDER
 6 <120> TITLE OF INVENTION: PROCESS FOR UTILIZING EPITOPES RECOGNIZED BY NATURAL
 ANTIBODIES
 8 <130> FILE REFERENCE: MIRUS.014.02
 10 <140> CURRENT APPLICATION NUMBER: 09/559021A
 11 <141> CURRENT FILING DATE: 2000-04-27
 13 <160> NUMBER OF SEQ ID NOS: 125
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 11
 19 <212> TYPE: PRT
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 25 1 5 10
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 29 <211> LENGTH: 27
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 31 <213> ORGANISM: Bacteriophage T7
 33 <400> SEQUENCE: 2
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 39 Arg Gln Ser Gly Arg Gly Lys Ser Ser Arg Pro
 40 20 25
 43 <210> SEQ ID NO: 3
 44 <211> LENGTH: 23
 45 <212> TYPE: PRT
 46 <213> ORGANISM: Bacteriophage T7
 48 <400> SEQUENCE: 3
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 51 1 5 10 15
 54 Lys Leu Ala Ala Ala Leu Glu
 55 20
 58 <210> SEQ ID NO: 4
 59 <211> LENGTH: 8
 60 <212> TYPE: PRT
 61 <213> ORGANISM: Bacteriophage T7
 63 <400> SEQUENCE: 4
 65 Ala Ala Gly Ala Val Val Phe Gln
 66 1 5
 69 <210> SEQ ID NO: 5
 70 <211> LENGTH: 343
 71 <212> TYPE: PRT

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72 <213> ORGANISM: Bacteriophage T7

74 <400> SEQUENCE: 5

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77 1          5          10          15
80 Gly Val Val Ala Ala Gly Asp Lys Leu Ala Leu Phe Leu Lys Val Phe
81          20          25          30
84 Gly Gly Glu Val Leu Thr Ala Phe Ala Arg Thr Ser Val Thr Thr Ser
85          35          40          45
88 Arg His Met Val Arg Ser Ile Ser Ser Gly Lys Ser Ala Gln Phe Pro
89          50          55          60
92 Val Leu Gly Arg Thr Gln Ala Ala Tyr Leu Ala Pro Gly Glu Asn Leu
93 65          70          75          80
96 Asp Asp Lys Arg Lys Asp Ile Lys His Thr Glu Lys Val Ile Thr Ile
97          85          90          95
100 Asp Gly Leu Leu Thr Ala Asp Val Leu Ile Tyr Asp Ile Glu Asp Ala
101          100          105          110
104 Met Asn His Tyr Asp Val Arg Ser Glu Tyr Thr Ser Gln Leu Gly Glu
105          115          120          125
108 Ser Leu Ala Met Ala Ala Asp Gly Ala Val Leu Ala Glu Ile Ala Gly
109          130          135          140
112 Leu Cys Asn Val Glu Ser Lys Tyr Asn Glu Asn Ile Glu Gly Leu Gly
113 145          150          155          160
116 Thr Ala Thr Val Ile Glu Thr Thr Gln Asn Lys Ala Ala Leu Thr Asp
117          165          170          175
120 Gln Val Ala Leu Gly Lys Glu Ile Ile Ala Ala Leu Thr Lys Ala Arg
121          180          185          190
124 Ala Ala Leu Thr Lys Asn Tyr Val Pro Ala Ala Asp Arg Val Phe Tyr
125          195          200          205
128 Cys Asp Pro Asp Ser Tyr Ser Ala Ile Leu Ala Ala Leu Met Pro Asn
129          210          215          220
132 Ala Ala Asn Tyr Ala Ala Leu Ile Asp Pro Glu Lys Gly Ser Ile Arg
133 225          230          235          240
136 Asn Val Met Gly Phe Glu Val Val Glu Val Pro His Leu Thr Ala Gly
137          245          250          255
140 Gly Ala Gly Thr Ala Arg Glu Gly Thr Thr Gly Gln Lys His Val Phe
141          260          265          270
144 Pro Ala Asn Lys Gly Glu Gly Asn Val Lys Val Ala Lys Asp Asn Val
145          275          280          285
148 Ile Gly Leu Phe Met His Arg Ser Ala Val Gly Thr Val Lys Leu Arg
149          290          295          300
152 Asp Leu Ala Leu Glu Arg Ala Arg Arg Ala Asn Phe Gln Ala Asp Gln
153 305          310          315          320
156 Ile Ile Ala Lys Tyr Ala Met Gly His Gly Gly Leu Arg Pro Glu Ala
157          325          330          335
160 Ala Gly Ala Val Val Phe Gln
161          340
164 <210> SEQ ID NO: 6
165 <211> LENGTH: 9
166 <212> TYPE: PRT

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167 <213> ORGANISM: Bacteriophage T7
169 <400> SEQUENCE: 6
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183 1 5 10
186 <210> SEQ ID NO: 8
187 <211> LENGTH: 9
188 <212> TYPE: PRT
189 <213> ORGANISM: Bacteriophage T7
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193 Glu Ala Ala Gly Ala Val Val Phe Gln
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197 <210> SEQ ID NO: 9
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202 <400> SEQUENCE: 9
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211 <213> ORGANISM: phage SV40
213 <400> SEQUENCE: 10
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219 His Ser Thr Pro Pro Lys Lys Lys Arg Lys Val Glu Asp Pro Lys Asp
220 20 25 30
223 Phe Pro Ser Glu Leu Leu Ser
224 35
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238 Ser Thr Pro Pro Lys Lys Lys Arg Lys Val Glu Asp Pro Lys Asp Phe
239 20 25 30
242 Pro Ser Glu Leu Leu Ser
243 35
246 <210> SEQ ID NO: 12
247 <211> LENGTH: 32

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Input Set : A:\Mirus.014.02.ST25.txt

Output Set: N:\CRF3\03112002\I559021A.raw

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248 <212> TYPE: PRT
249 <213> ORGANISM: M9 Protein
251 <400> SEQUENCE: 12
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254 1 5 10 15
257 Pro Met Lys Gln Gly Gly Asn Phe Gly Gly Arg Ser Ser Gly Pro Tyr
258 20 25 30
261 <210> SEQ ID NO: 13
262 <211> LENGTH: 10
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266 <400> SEQUENCE: 13
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269 1 5 10
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273 <211> LENGTH: 22
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275 <213> ORGANISM: Nucleoplasmin
277 <400> SEQUENCE: 14
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280 1 5 10 15
283 Ala Lys Lys Lys Lys Leu
284 20
287 <210> SEQ ID NO: 15
288 <211> LENGTH: 14
289 <212> TYPE: PRT
290 <213> ORGANISM: c-myc
292 <400> SEQUENCE: 15
294 Cys Lys Lys Lys Gly Pro Ala Ala Lys Arg Val Lys Leu Asp
295 1 5 10
298 <210> SEQ ID NO: 16
299 <211> LENGTH: 4
300 <212> TYPE: PRT
301 <213> ORGANISM: Bacteriophage T7
303 <400> SEQUENCE: 16
305 Phe Ser Gln Val
306 1
309 <210> SEQ ID NO: 17
310 <211> LENGTH: 4
311 <212> TYPE: PRT
312 <213> ORGANISM: endoplasmic reticulum proteins
314 <400> SEQUENCE: 17
316 Lys Asp Glu Leu
317 1
320 <210> SEQ ID NO: 18
321 <211> LENGTH: 4
322 <212> TYPE: PRT
323 <213> ORGANISM: Bacteriophage T7
325 <400> SEQUENCE: 18

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Input Set : A:\Mirus.014.02.ST25.txt

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327 Gln Val Thr Lys
328 1
331 <210> SEQ ID NO: 19
332 <211> LENGTH: 8
333 <212> TYPE: PRT
334 <213> ORGANISM: Bacteriophage T7
336 <400> SEQUENCE: 19
338 Val Val Val Glu Ser Val Pro Lys
339 1 5
342 <210> SEQ ID NO: 20
343 <211> LENGTH: 6
344 <212> TYPE: PRT
345 <213> ORGANISM: Bacteriophage T7
347 <400> SEQUENCE: 20
349 Ala Arg Pro Val Gln Lys
350 1 5
353 <210> SEQ ID NO: 21
354 <211> LENGTH: 8
355 <212> TYPE: PRT
356 <213> ORGANISM: Bacteriophage T7
358 <400> SEQUENCE: 21
360 Gln Leu Val Arg Val Ile Ser Arg
361 1 5
364 <210> SEQ ID NO: 22
365 <211> LENGTH: 4
366 <212> TYPE: PRT
367 <213> ORGANISM: Bacteriophage T7
369 <400> SEQUENCE: 22
371 Gly Arg Leu Lys
372 1
375 <210> SEQ ID NO: 23
376 <211> LENGTH: 5
377 <212> TYPE: PRT
378 <213> ORGANISM: Bacteriophage T7
380 <400> SEQUENCE: 23
382 Ala Phe Thr Asn Lys
383 1 5
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387 <211> LENGTH: 6
388 <212> TYPE: PRT
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394 1 5
397 <210> SEQ ID NO: 25
398 <211> LENGTH: 7
399 <212> TYPE: PRT
400 <213> ORGANISM: Bacteriophage T7
402 <400> SEQUENCE: 25

VERIFICATION SUMMARY

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